

OM nucleic - nucleic search, using sw model

Run on: April 16, 2004, 05:43:00 ; Search time 4542.67 Seconds  
(without alignments)  
*encodes SEQ:1* 10485.907 Million cell updates/sec

Title: US-08-737-319-4 *in DNA databases*  
Perfect score: 1099  
Sequence: 1 CCCACGCGTCCGCACATCTC.....ACTACAAAAAAAAAAAAAAAAA 1099

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*

*exact DNA SEQ4*

28: em\_un:\*  
 29: em\_vi:\*  
 30: em\_htg\_hum:\*  
 31: em\_htg\_inv:\*  
 32: em\_htg\_other:\*  
 33: em\_htg\_mus:\*  
 34: em\_htg\_pln:\*  
 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1099	100.0	1099	6	E12045 JP 1996 242861	E12045 cDNA encodi
2	1099	100.0	1099	6	BD014674 JP 2001 136792	BD014674 Method of
3	1084	98.610	1084	8	AB019035 1997 GenBank - AB019035	Xanthophy
4	1071.6	97.5	1165	6	A63895 60 97/23633	A63895 Sequence 20
5	1071.6	97.5	1165	6	AR366158 USPN 6329141	AR366158 Sequence
6	556.2	50.6	3239	8	PRY15811	Y15811 Xanthophyll
7	161.8	14.7	1017	8	AF479816	AF479816 Aspergill
8	128	11.6	990	8	BT009297	BT009297 Triticum
9	126.2	11.5	931	8	SPU21154	U21154 Schizosacch
10	125	11.4	1002	6	AR428557	AR428557 Sequence
11	125	11.4	1002	6	BD223741	BD223741 Genes of
12	125	11.4	1002	8	AF188061	AF188061 Adonis pa
13	124.2	11.3	1270	6	AR428558	AR428558 Sequence
14	124.2	11.3	1270	8	AF188060	AF188060 Adonis pa
15	124.2	11.3	1271	6	BD223742	BD223742 Genes of
16	123.8	11.3	1207	8	CBIPISOM	X82627 C.breweri m
17	123.2	11.2	1095	8	AF330034	AF330034 Zea mays
18	121.6	11.1	600	8	AY290736	AY290736 Triticum
19	121.4	11.0	1031	6	AR428564	AR428564 Sequence
20	121.4	11.0	1031	6	BD223748	BD223748 Genes of
21	121.4	11.0	1031	8	AF188065	AF188065 Oryza sat
22	121.4	11.0	1101	8	AK061800	AK061800 Oryza sat
23	121.4	11.0	1108	8	AK065871	AK065871 Oryza sat
24	119.6	10.9	1139	8	AF031079	AF031079 Camptothe
25	118	10.7	1225	8	AF483191	AF483191 Melaleuca
26	117.8	10.7	1028	8	AB041629	AB041629 Eucommia
27	117.4	10.7	1063	8	AF483190	AF483190 Melaleuca
28	114.8	10.4	985	6	AR428560	AR428560 Sequence
29	114.8	10.4	985	6	BD223744	BD223744 Genes of
30	114.8	10.4	985	8	AF188062	AF188062 Lactuca s
31	114.4	10.4	956	6	AR428563	AR428563 Sequence
32	114.2	10.4	1053	8	AF236092	AF236092 Brassica
33	113.2	10.3	956	8	AF188064	AF188064 Tagetes e

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OM nucleic - nucleic search, using sw model

Run on: April 16, 2004, 05:39:50 ; Search time 517.385 Seconds  
(without alignments)  
9023.787 Million cell updates/sec

Title: US-08-737-319-4  
Perfect score: 1099  
Sequence: 1 CCCACGCGTCCGCACATCTC.....ACTACAAAAAAAAAAAAAAAAA 1099

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result	% Query					
No.	Score	Match Length DB ID	Description			
1	1088	99.0 1100 2	AAT40216	4096/28545	Aat40216 Sequence	
2	1071.6	97.5 1165 2	AAT72945	4077/23633	Aat72945 Phaffia c	
3	202.6	18.4 846 9	ADB69660		Adb69660 C. neoformans	
4	182.2	16.6 816 7	ABT19254		Abt19254 Aspergillus	
5	179	16.3 816 7	ABT21074		Abt21074 Aspergillus	
6	139.2	12.7 698 3	AAF14664		Aaf14664 Aspergillus	
7	126.2	11.5 684 6	AAD31019		Aad31019 Schizosaccharomyces	

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OM nucleic - nucleic search, using sw model

Run on: April 16, 2004, 07:53:36 ; Search time 3328.36 Seconds  
(without alignments)  
9860.282 Million cell updates/sec

Title: US-08-737-319-4  
Perfect score: 1099  
Sequence: 1 CCCACGCGTCCGCACATCTC.....ACTACAAAAAAAAAAAAAAAA 1099

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*

28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	%		Query			ID	Description
	No.	Score	Match	Length	DB		
c	1	170	15.5	762	14	CF869867	CF869867 tric020xl
	2	170	15.5	817	14	CB900020	CB900020 tric020xl
	3	166.6	15.2	753	14	CF873428	CF873428 tric033xc
	4	166.6	15.2	824	14	CB903168	CB903168 tric033xc
	5	165.6	15.1	988	14	CF883213	CF883213 tric033xc
	6	158.6	14.4	1051	29	CNS076H2	AL431388 T3 end of
	7	157.8	14.4	969	14	CD456156	CD456156 Fg03_08f1
	8	156.2	14.2	729	13	BX867082	BX867082 BX867082
	9	155.6	14.2	671	14	CA373519	CA373519 647675 NC
	10	143.2	13.0	729	14	CF883402	CF883402 tric088xh
	11	143.2	13.0	789	14	CB909533	CB909533 tric088xh
	12	141	12.8	882	11	CNS09LQ8	BX064236 Single re
	13	141	12.8	1006	11	CNS097QT	BX046113 Single re
	14	141	12.8	1024	11	CNS098Q1	BX047381 Single re
	15	140.8	12.8	1219	14	CD497570	CD497570 CDA28-F04
	16	139.4	12.7	1003	11	CNS09J4Q	BX060870 Single re
	17	139.2	12.7	711	14	CF524263	CF524263 AGENCOURT
	18	139	12.6	864	13	BX721162	BX721162 BX721162
	19	139	12.6	881	13	BX743804	BX743804 BX743804
	20	139	12.6	890	13	BX718091	BX718091 BX718091
c	21	138.6	12.6	1051	14	CD507557	CD507557 CDA85-H04
	22	137.2	12.5	836	14	CF592215	CF592215 AGENCOURT
	23	134.6	12.2	976	11	CNS098Q2	BX047382 Single re
	24	134.4	12.2	748	14	CF996558	CF996558 AGENCOURT
	25	133	12.1	795	11	CNS09EKB	BX054951 Single re
	26	133	12.1	819	11	CNS095N2	BX043386 Single re
	27	131.6	12.0	686	13	CA081651	CA081651 SCAGAM201
	28	131.4	12.0	918	11	CNS097QU	BX046114 Single re
	29	131.4	12.0	949	11	CNS09ARG	BX050024 Single re
	30	131.2	11.9	679	14	CD909408	CD909408 G468.112J
	31	131.2	11.9	682	12	BJ317597	BJ317597 BJ317597
	32	131.2	11.9	689	13	BU100341	BU100341 WHE3352_B
	33	131.2	11.9	779	13	BU100364	BU100364 WHE3352_D
	34	131	11.9	777	13	BX853590	BX853590 BX853590
	35	131	11.9	804	13	CA125145	CA125145 SCRFLR101
	36	129.6	11.8	676	12	BG605474	BG605474 WHE2332_C
	37	129.6	11.8	794	13	BQ806442	BQ806442 WHE3579_B
	38	129.4	11.8	680	13	CA066701	CA066701 SCEQAD101
	39	129.2	11.8	624	14	CA732092	CA732092 wlp1c.pk0
	40	129.2	11.8	931	14	CD253449	CD253449 AGENCOURT
	41	129	11.7	571	9	AV602890	AV602890 AV602890
	42	128.4	11.7	640	14	CD496124	CD496124 CDA20-E07
	43	128.2	11.7	646	14	CB059459	CB059459 4008699 B
	44	128	11.6	636	12	BJ223696	BJ223696 BJ223696
	45	128	11.6	717	13	BQ483516	BQ483516 WHE3509_E

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OM nucleic - nucleic search, using sw model

Run on: April 16, 2004, 08:14:02 ; Search time 103.679 Seconds  
(without alignments)  
5882.479 Million cell updates/sec

Title: US-08-737-319-4  
Perfect score: 1099  
Sequence: 1 CCCACGCGTCCGCACATCTC.....ACTACAAAAAAAAAAAAAAAAA 1099

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1071.6	97.5	1165	4	US-09-091-725-20	Sequence 20, Appl
2	125	11.4	1002	4	US-09-323-998E-28	Sequence 28, Appl
3	124.2	11.3	1270	4	US-09-323-998E-29	Sequence 29, Appl
4	121.4	11.0	1031	4	US-09-323-998E-35	Sequence 35, Appl
5	114.8	10.4	985	4	US-09-323-998E-31	Sequence 31, Appl
6	114.4	10.4	956	4	US-09-323-998E-34	Sequence 34, Appl
7	111.6	10.2	1020	3	US-09-201-641-7	Sequence 7, Appli
8	109.4	10.0	954	1	US-08-624-125-9	Sequence 9, Appli
9	109.4	10.0	954	4	US-08-937-155-9	Sequence 9, Appli
10	109.4	10.0	954	4	US-09-323-998E-9	Sequence 9, Appli
11	109.4	10.0	996	1	US-08-624-125-10	Sequence 10, Appl

USPN 6329141

OM nucleic - nucleic search, using sw model

Run on: April 16, 2004, 07:53:36 ; Search time 3252.64 Seconds  
(without alignments)  
*encodes SEQ:2* 9860.282 Million cell updates/sec

Title: US-08-737-319<sup>(5)</sup> *in DNA databases*  
Perfect score: 1074  
Sequence: 1 ATCGCTACTTGGAACTGGC.....CTGGAAAAAAAAAAAAAAAA 1074

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pln:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_mam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vrl:\*

*exact DNA SEQ:5*

28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	119.8	11.2	988	14	CF883213	CF883213	tric033xc
2	117.8	11.0	753	14	CF873428	CF873428	tric033xc
3	117.8	11.0	824	14	CB903168	CB903168	tric033xc
4	115	10.7	729	14	CF883402	CF883402	tric088xh
5	115	10.7	789	14	CB909533	CB909533	tric088xh
6	110.4	10.3	762	14	CF869867	CF869867	tric020xl
7	110.4	10.3	817	14	CB900020	CB900020	tric020xl
8	108.6	10.1	696	14	CD881481	CD881481	F1.103F22
9	108.6	10.1	852	12	BG418760	BG418760	HVSMEk002
10	108.4	10.1	969	14	CD456156	CD456156	Fg03_08f1
11	108	10.1	717	13	BQ483516	BQ483516	WHE3509_E
12	107.2	10.0	694	14	CB679092	CB679092	OSJNEf02C
13	106.4	9.9	782	13	BQ802836	BQ802836	WHE2830_E
14	104.8	9.8	584	13	BU987666	BU987666	HF15G16r
15	104.8	9.8	636	12	BJ223696	BJ223696	BJ223696
16	104.8	9.8	710	14	CB685009	CB685009	OSJNEf15B
17	104.8	9.8	794	13	BQ806442	BQ806442	WHE3579_B
18	104.8	9.8	825	10	BF254179	BF254179	HVSMEf000
19	104.8	9.8	889	12	BM816948	BM816948	HB106H05_
20	103.2	9.6	676	12	BG605474	BG605474	WHE2332_C
21	103.2	9.6	682	12	BJ317597	BJ317597	BJ317597
22	103.2	9.6	689	13	BU100341	BU100341	WHE3352_B
23	103.2	9.6	779	13	BU100364	BU100364	WHE3352_D
24	103.2	9.6	1168	14	CK171569	CK171569	FGAS04688
25	102.2	9.5	1193	11	AY104380	AY104380	Zea mays
26	101.6	9.5	679	14	CD909408	CD909408	G468.112J
27	101.6	9.5	702	10	BF628760	BF628760	HVSMEb000
28	100.6	9.4	627	10	BE444992	BE444992	WHE1130_H
29	98.8	9.2	549	13	BU984464	BU984464	HF04A18r
30	96.4	9.0	659	12	BI955926	BI955926	HVSMEm002
31	94.8	8.8	676	14	CB092421	CB092421	hf05e09.g
32	94.6	8.8	624	14	CA732092	CA732092	wlp1c.pk0
33	94.4	8.8	397	14	CB210679	CB210679	OML00959
c 34	94.4	8.8	708	9	AU094436	AU094436	AU094436
35	94.2	8.8	516	12	BJ557662	BJ557662	BJ557662
36	94.2	8.8	563	12	BJ563607	BJ563607	BJ563607
37	92.8	8.6	671	14	CA754492	CA754492	BR0400180
38	91	8.5	410	12	BG558356	BG558356	RHIZ2_66_
39	91	8.5	579	12	BM868602	BM868602	mgns001xM
40	90.8	8.5	602	14	CB076830	CB076830	hj45c01.g
41	90.8	8.5	655	14	CB076704	CB076704	hj43d10.g
42	90.8	8.5	747	13	BU100120	BU100120	WHE3315_D
43	90.6	8.4	351	9	AV413323	AV413323	AV413323
44	90.6	8.4	398	9	AV412565	AV412565	AV412565
45	90.6	8.4	413	9	AV424051	AV424051	AV424051



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OM nucleic - nucleic search, using sw model

Run on: April 16, 2004, 05:43:00 ; Search time 4439.33 Seconds  
(without alignments)  
10485.907 Million cell updates/sec

Title: US-08-737-319-5  
Perfect score: 1074  
Sequence: 1 ATCGCTACTTGAACCTGGC.....CTGGAAAAAAAAAAAAAAAA 1074

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*

28: em\_un:\*  
 29: em\_vi:\*  
 30: em\_htg\_hum:\*  
 31: em\_htg\_inv:\*  
 32: em\_htg\_other:\*  
 33: em\_htg\_mus:\*  
 34: em\_htg\_pln:\*  
 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	1074	100.0	1074	6	E12046	JP 1996242861	E12046 cDNA encodi	
	2	1074	100.0	1074	6	BD014675	JP 2001136992	BD014675 Method of	
	3	1058	<del>98.5</del> 100	1058	8	AB019034	1997	AB019034 Haematoco	
	4	931	86.7	1099	8	AF082326		AF082326 Haematoco	
	5	931	86.7	1109	6	AR428559		AR428559 Sequence	
	6	931	86.7	1109	6	BD223743		BD223743 Genes of	
	7	925.6	86.2	1135	6	AR003639		AR003639 Sequence	
	8	925.6	86.2	1135	6	AR428553		AR428553 Sequence	
	9	925.6	86.2	1135	6	BD223737		BD223737 Genes of	
	10	878	81.8	1150	8	AF082325		AF082325 Haematoco	
	11	878	81.8	1165	6	AR003638		AR003638 Sequence	
	12	878	81.8	1165	6	AR428552		AR428552 Sequence	
	13	878	81.8	1165	6	BD223736		BD223736 Genes of	
	14	236.2	22.0	1860	8	AF082869		AF082869 Chlamydom	
	15	236.2	22.0	1874	6	AR428562		AR428562 Sequence	
	16	236.2	22.0	1874	6	BD223746		BD223746 Genes of	
	17	107.2	10.0	1031	6	AR428564		AR428564 Sequence	
	18	107.2	10.0	1031	6	BD223748		BD223748 Genes of	
	19	107.2	10.0	1031	8	AF188065		AF188065 Oryza sat	
	20	107.2	10.0	1101	8	AK061800		AK061800 Oryza sat	
	21	107.2	10.0	1108	8	AK065871		AK065871 Oryza sat	
	22	106.8	9.9	1017	8	AF479816		AF479816 Aspergill	
	23	104.8	9.8	990	8	BT009297		BT009297 Triticum	
	24	97.4	9.1	989	8	AK099027		AK099027 Oryza sat	
	25	97.4	9.1	1082	8	AK060336		AK060336 Oryza sat	
	26	93.6	8.7	1028	8	AB041629		AB041629 Eucommia	
	27	91	8.5	412	6	BD272976		BD272976 Materials	
	28	90.8	8.5	301675	1	AP005027		AP005027 Streptomy	
	29	86.8	8.1	1063	8	AF483190		AF483190 Melaleuca	
	30	86.2	8.0	1095	8	AF330034		AF330034 Zea mays	
	31	85.6	8.0	1139	8	AF031079		AF031079 Camptothe	
c	32	85.6	8.0	292200	1	SCO939129		AL939129 Streptomy	
	33	85.2	7.9	927	3	AY118469		AY118469 Drosophil	

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1074	100.0	1134	2	AAT40217	Aat40217 Sequence
2	931	86.7	1109	3	AAZ45589	Aaz45589 Nucleotid
3	931	86.7	1109	6	ABS71577	Abs71577 H. pluvia
4	925.6	86.2	1135	2	AAT95391	Aat95391 Haematoco
5	925.6	86.2	1135	3	AAZ45583	Aaz45583 cDNA enco
6	925.6	86.2	1135	6	ABS71571	Abs71571 H. pluvia
7	878	81.8	1165	2	AAT95390	Aat95390 Haematoco

OM nucleic - nucleic search, using sw model

Run on: April 16, 2004, 08:14:02 ; Search time 101.321 Seconds  
 (without alignments)  
 5882.479 Million cell updates/sec

Title: US-08-737-319-5  
 Perfect score: 1074  
 Sequence: 1 ATCGCTACTTGGAACTTGGC.....CTGGAAAAAAAAAAAAAAAAA 1074

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	931	86.7	1109	4	US-09-323-998E-30	Sequence 30, Appl
2	925.6	86.2	1135	1	US-08-624-125-12	Sequence 12, Appl
3	925.6	86.2	1135	4	US-08-937-155-12	Sequence 12, Appl
4	925.6	86.2	1135	4	US-09-323-998E-12	Sequence 12, Appl
5	878	81.8	1165	1	US-08-624-125-11	Sequence 11, Appl
6	878	81.8	1165	4	US-08-937-155-11	Sequence 11, Appl
7	878	81.8	1165	4	US-09-323-998E-11	Sequence 11, Appl
8	236.2	22.0	1874	4	US-09-323-998E-33	Sequence 33, Appl
9	107.2	10.0	1031	4	US-09-323-998E-35	Sequence 35, Appl
10	82	7.6	996	1	US-08-624-125-10	Sequence 10, Appl
11	82	7.6	996	4	US-08-937-155-10	Sequence 10, Appl